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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/259,389

 DATE: 03/15/1999
 TIME: 14:17:32

Input Set: I259389.RAW

 This Raw Listing contains the General Information
 Section and up to first 5 pages.

ENTERED

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1  <110> APPLICANT: Georgopoulos, Katia
2      Mogan, Bruce A.
3      Kelly, Clair
4  <120> TITLE OF INVENTION: THE HELIOS GENE
5  <130> FILE REFERENCE: 10287/043001
6  <140> CURRENT APPLICATION NUMBER: US/09/259,389
7  <141> CURRENT FILING DATE: 1999-02-26
8  <150> EARLIER APPLICATION NUMBER: US 60/076,325
9  <151> EARLIER FILING DATE: 1998-02-27
10 <160> NUMBER OF SEQ ID NOS: 17
11 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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13 <211> LENGTH: 1598
14 <212> TYPE: DNA
15 <213> ORGANISM: Mus musculus
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22          1              5              10              15
23      tca ccc gaa ggg gaa cac gcc aat atg gcc att gac ctc acc tca agc      96
24      Ser Pro Glu Gly Glu His Ala Asn Met Ala Ile Asp Leu Thr Ser Ser
25          20              25              30
26      acg ccc aat gga cag cac gcc tcg cca agt cac atg aca agc aca aat      144
27      Thr Pro Asn Gly Gln His Ala Ser Pro Ser His Met Thr Ser Thr Asn
28          35              40              45
29      tct gta aag ctg gaa atg cag agt gat gaa gag tgt gac agg cag ccc      192
30      Ser Val Lys Leu Glu Met Gln Ser Asp Glu Glu Cys Asp Arg Gln Pro
31          50              55              60
32      ctg agc cgt gag gat gag atc agg ggc cac gat gag ggg agc agc cta      240
33      Leu Ser Arg Glu Asp Glu Ile Arg Gly His Asp Glu Gly Ser Ser Leu
34          65              70              75              80
35      gaa gaa ccc cta att gag agc agc gag gtg gcc gac aac agg aaa gtc      288
36      Glu Glu Pro Leu Ile Glu Ser Ser Glu Val Ala Asp Asn Arg Lys Val
37          85              90              95
38      cag gac ctt caa ggc gag gga gga atc cgg ctt ccg aat ggt aaa ctg      336
39      Gln Asp Leu Gln Gly Glu Gly Gly Ile Arg Leu Pro Asn Gly Lys Leu
40          100             105             110
41      aaa tgt gac gtc tgt ggc atg gtt tgc att ggg ccc aat gtg ctt atg      384
42      Lys Cys Asp Val Cys Gly Met Val Cys Ile Gly Pro Asn Val Leu Met
43          115             120             125
44      gta cat aaa agg agt cac act ggt gag cgg ccc ttc cac tgt aac cag      432

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45	Val	His	Lys	Arg	Ser	His	Thr	Gly	Glu	Arg	Pro	Phe	His	Cys	Asn	Gln	
46		130					135					140					
47	tgc	gga	gct	tct	ttt	acc	cag	aag	ggc	aac	ctt	ctg	aga	cac	ata	aag	480
48	Cys	Gly	Ala	Ser	Phe	Thr	Gln	Lys	Gly	Asn	Leu	Leu	Arg	His	Ile	Lys	
49		145				150				155					160		
50	tta	cac	tct	gga	gag	aag	ccc	ttc	aaa	tgt	cct	ttc	tgt	agc	tat	gct	528
51	Leu	His	Ser	Gly	Glu	Lys	Pro	Phe	Lys	Cys	Pro	Phe	Cys	Ser	Tyr	Ala	
52					165				170						175		
53	tgt	aga	aga	agg	gac	gct	ctc	aca	gga	cac	ctc	agg	acc	cat	tct	gtg	576
54	Cys	Arg	Arg	Arg	Asp	Ala	Leu	Thr	Gly	His	Leu	Arg	Thr	His	Ser	Val	
55				180					185					190			
56	ggt	aaa	cct	cac	aag	tgt	aac	tac	tgt	ggc	cga	agc	tac	aag	cag	cgc	624
57	Gly	Lys	Pro	His	Lys	Cys	Asn	Tyr	Cys	Gly	Arg	Ser	Tyr	Lys	Gln	Arg	
58			195					200					205				
59	acg	tca	ctg	gag	gaa	cac	aag	gaa	cgc	tgt	cac	aac	tat	ctc	cag	aat	672
60	Thr	Ser	Leu	Glu	Glu	His	Lys	Glu	Arg	Cys	His	Asn	Tyr	Leu	Gln	Asn	
61		210					215					220					
62	gtc	agc	atg	gag	gct	gcc	ggg	cag	gtc	atg	agt	cac	cat	gta	ccg	cct	720
63	Val	Ser	Met	Glu	Ala	Ala	Gly	Gln	Val	Met	Ser	His	His	Val	Pro	Pro	
64		225				230				235					240		
65	atg	gaa	gat	tgt	aag	gaa	caa	gag	cct	atc	atg	gac	aac	aat	att	tct	768
66	Met	Glu	Asp	Cys	Lys	Glu	Gln	Glu	Pro	Ile	Met	Asp	Asn	Asn	Ile	Ser	
67				245					250					255			
68	ctg	gtg	cct	ttt	gag	aga	cct	gct	gtc	ata	gag	aag	ctc	acg	gca	aat	816
69	Leu	Val	Pro	Phe	Glu	Arg	Pro	Ala	Val	Ile	Glu	Lys	Leu	Thr	Ala	Asn	
70			260						265					270			
71	atg	gga	aag	cgc	aaa	agc	tcc	act	cct	cag	aag	ttt	gtg	ggg	gaa	aag	864
72	Met	Gly	Lys	Arg	Lys	Ser	Ser	Thr	Pro	Gln	Lys	Phe	Val	Gly	Glu	Lys	
73			275					280					285				
74	ctt	atg	cga	ttc	agc	tac	cca	gat	att	cat	ttt	gat	atg	aac	tta	aca	912
75	Leu	Met	Arg	Phe	Ser	Tyr	Pro	Asp	Ile	His	Phe	Asp	Met	Asn	Leu	Thr	
76		290					295				300						
77	tat	gag	aag	gag	gct	gag	ctg	atg	cag	tct	cat	atg	atg	gac	caa	gcc	960
78	Tyr	Glu	Lys	Glu	Ala	Glu	Leu	Met	Gln	Ser	His	Met	Met	Asp	Gln	Ala	
79		305				310					315				320		
80	atc	aac	aat	gca	atc	acc	tac	ctt	gga	gct	gag	gcc	ctt	cac	cct	ctg	1008
81	Ile	Asn	Asn	Ala	Ile	Thr	Tyr	Leu	Gly	Ala	Glu	Ala	Leu	His	Pro	Leu	
82				325					330					335			
83	atg	cag	cat	gca	cca	agc	aca	atc	gct	gag	gtg	gcc	cca	gtt	ata	agc	1056
84	Met	Gln	His	Ala	Pro	Ser	Thr	Ile	Ala	Glu	Val	Ala	Pro	Val	Ile	Ser	
85			340						345					350			
86	tca	gct	tat	tct	cag	gtc	tat	cat	cca	aac	agg	ata	gaa	aga	ccc	att	1104
87	Ser	Ala	Tyr	Ser	Gln	Val	Tyr	His	Pro	Asn	Arg	Ile	Glu	Arg	Pro	Ile	
88		355					360					365					
89	agc	agg	gaa	aca	tct	gat	agt	cac	gaa	aac	aac	atg	gat	ggc	ccc	atc	1152
90	Ser	Arg	Glu	Thr	Ser	Asp	Ser	His	Glu	Asn	Asn	Met	Asp	Gly	Pro	Ile	
91		370					375					380					
92	tct	ctc	atc	aga	cca	aag	agt	cga	ccc	cag	gaa	aga	gag	gcc	tcg	ccc	1200
93	Ser	Leu	Ile	Arg	Pro	Lys	Ser	Arg	Pro	Gln	Glu	Arg	Glu	Ala	Ser	Pro	
94		385				390				395					400		

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95	agc aat agc tgc ctc gat tct act gac tca gaa agt agc cat gat gac	1248
96	Ser Asn Ser Cys Leu Asp Ser Thr Asp Ser Glu Ser Ser His Asp Asp	
97	405 410 415	
98	cgc cag tcc tac caa gga aac cct gcc tta aat ccc aag agg aaa caa	1296
99	Arg Gln Ser Tyr Gln Gly Asn Pro Ala Leu Asn Pro Lys Arg Lys Gln	
100	420 425 430	
101	agc cca gct tac atg aag gag gat gtc aag gct ttg gat gct acc aag	1344
102	Ser Pro Ala Tyr Met Lys Glu Asp Val Lys Ala Leu Asp Ala Thr Lys	
103	435 440 445	
104	gcc ccc aag ggc tct ctg aag gac atc tat aag gtt ttc aat gga gaa	1392
105	Ala Pro Lys Gly Ser Leu Lys Asp Ile Tyr Lys Val Phe Asn Gly Glu	
106	450 455 460	
107	gga gaa cag ata agg gcc ttc aag tgt gag cac tgc cga gtc ctt ttt	1440
108	Gly Glu Gln Ile Arg Ala Phe Lys Cys Glu His Cys Arg Val Leu Phe	
109	465 470 475 480	
110	cta gac cat gtc atg tac acc att cac atg ggt tgc cat ggc tac cgg	1488
111	Leu Asp His Val Met Tyr Thr Ile His Met Gly Cys His Gly Tyr Arg	
112	485 490 495	
113	gac cca ctg gaa tgc aac atc tgt ggc tac aga agc cag gac cgc tac	1536
114	Asp Pro Leu Glu Cys Asn Ile Cys Gly Tyr Arg Ser Gln Asp Arg Tyr	
115	500 505 510	
116	gaa ttt tca tca cac att gtt ggg ggg cag cac aca ttc cac	1578
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123	<213> ORGANISM: Mus musculus	
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128	20 25 30	
129	Thr Pro Asn Gly Gln His Ala Ser Pro Ser His Met Thr Ser Thr Asn	
130	35 40 45	
131	Ser Val Lys Leu Glu Met Gln Ser Asp Glu Glu Cys Asp Arg Gln Pro	
132	50 55 60	
133	Leu Ser Arg Glu Asp Glu Ile Arg Gly His Asp Glu Gly Ser Ser Leu	
134	65 70 75 80	
135	Glu Glu Pro Leu Ile Glu Ser Ser Glu Val Ala Asp Asn Arg Lys Val	
136	85 90 95	
137	Gln Asp Leu Gln Gly Glu Gly Gly Ile Arg Leu Pro Asn Gly Lys Leu	
138	100 105 110	
139	Lys Cys Asp Val Cys Gly Met Val Cys Ile Gly Pro Asn Val Leu Met	
140	115 120 125	
141	Val His Lys Arg Ser His Thr Gly Glu Arg Pro Phe His Cys Asn Gln	
142	130 135 140	
143	Cys Gly Ala Ser Phe Thr Gln Lys Gly Asn Leu Leu Arg His Ile Lys	
144	145 150 155 160	

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145      Leu His Ser Gly Glu Lys Pro Phe Lys Cys Pro Phe Cys Ser Tyr Ala
146                      165                      170                      175
147      Cys Arg Arg Arg Asp Ala Leu Thr Gly His Leu Arg Thr His Ser Val
148                      180                      185                      190
149      Gly Lys Pro His Lys Cys Asn Tyr Cys Gly Arg Ser Tyr Lys Gln Arg
150                      195                      200                      205
151      Thr Ser Leu Glu Glu His Lys Glu Arg Cys His Asn Tyr Leu Gln Asn
152                      210                      215                      220
153      Val Ser Met Glu Ala Ala Gly Gln Val Met Ser His His Val Pro Pro
154      225                      230                      235                      240
155      Met Glu Asp Cys Lys Glu Gln Glu Pro Ile Met Asp Asn Asn Ile Ser
156                      245                      250                      255
157      Leu Val Pro Phe Glu Arg Pro Ala Val Ile Glu Lys Leu Thr Ala Asn
158                      260                      265                      270
159      Met Gly Lys Arg Lys Ser Ser Thr Pro Gln Lys Phe Val Gly Glu Lys
160                      275                      280                      285
161      Leu Met Arg Phe Ser Tyr Pro Asp Ile His Phe Asp Met Asn Leu Thr
162      290                      295                      300
163      Tyr Glu Lys Glu Ala Glu Leu Met Gln Ser His Met Met Asp Gln Ala
164      305                      310                      315                      320
165      Ile Asn Asn Ala Ile Thr Tyr Leu Gly Ala Glu Ala Leu His Pro Leu
166                      325                      330                      335
167      Met Gln His Ala Pro Ser Thr Ile Ala Glu Val Ala Pro Val Ile Ser
168                      340                      345                      350
169      Ser Ala Tyr Ser Gln Val Tyr His Pro Asn Arg Ile Glu Arg Pro Ile
170                      355                      360                      365
171      Ser Arg Glu Thr Ser Asp Ser His Glu Asn Asn Met Asp Gly Pro Ile
172      370                      375                      380
173      Ser Leu Ile Arg Pro Lys Ser Arg Pro Gln Glu Arg Glu Ala Ser Pro
174      385                      390                      395                      400
175      Ser Asn Ser Cys Leu Asp Ser Thr Asp Ser Glu Ser Ser His Asp Asp
176                      405                      410                      415
177      Arg Gln Ser Tyr Gln Gly Asn Pro Ala Leu Asn Pro Lys Arg Lys Gln
178                      420                      425                      430
179      Ser Pro Ala Tyr Met Lys Glu Asp Val Lys Ala Leu Asp Ala Thr Lys
180                      435                      440                      445
181      Ala Pro Lys Gly Ser Leu Lys Asp Ile Tyr Lys Val Phe Asn Gly Glu
182      450                      455                      460
183      Gly Glu Gln Ile Arg Ala Phe Lys Cys Glu His Cys Arg Val Leu Phe
184      465                      470                      475                      480
185      Leu Asp His Val Met Tyr Thr Ile His Met Gly Cys His Gly Tyr Arg
186                      485                      490                      495
187      Asp Pro Leu Glu Cys Asn Ile Cys Gly Tyr Arg Ser Gln Asp Arg Tyr
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193      <212> TYPE: DNA
194      <213> ORGANISM: Mus musculus

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196 <221> NAME/KEY: CDS
197 <222> LOCATION: (1)...(1500)
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201         1             5             10             15
202     tca ccc gaa ggg gaa cac gcc aat atg gcc att gac ctc acc tca agc      96
203     Ser Pro Glu Gly Glu His Ala Asn Met Ala Ile Asp Leu Thr Ser Ser
204         20             25             30
205     acg ccc aat gga cag cac gcc tcg cca agt cac atg aca agc aca aat     144
206     Thr Pro Asn Gly Gln His Ala Ser Pro Ser His Met Thr Ser Thr Asn
207         35             40             45
208     tct gta aag ctg gaa atg cag agt gat gaa gag tgt gac agg cag ccc     192
209     Ser Val Lys Leu Glu Met Gln Ser Asp Glu Glu Cys Asp Arg Gln Pro
210         50             55             60
211     ctg agc cgt gag gat gag atc agg ggc cac gat gag ggg agc agc cta     240
212     Leu Ser Arg Glu Asp Glu Ile Arg Gly His Asp Glu Gly Ser Ser Leu
213         65             70             75             80
214     gaa gaa ccc cta att gag agc agc gag gtg gcc gac aac agg aaa gtc     288
215     Glu Glu Pro Leu Ile Glu Ser Ser Glu Val Ala Asp Asn Arg Lys Val
216         85             90             95
217     cag gac ctt caa ggc gag gga gga atc cgg ctt ccg aat ggt gag cgg     336
218     Gln Asp Leu Gln Gly Glu Gly Gly Ile Arg Leu Pro Asn Gly Glu Arg
219         100            105            110
220     ccc ttc cac tgt aac cag tgc gga gct tct ttt acc cag aag ggc aac     384
221     Pro Phe His Cys Asn Gln Cys Gly Ala Ser Phe Thr Gln Lys Gly Asn
222         115            120            125
223     ctt ctg aga cac ata aag tta cac tct gga gag aag ccc ttc aaa tgt     432
224     Leu Leu Arg His Ile Lys Leu His Ser Gly Glu Lys Pro Phe Lys Cys
225         130            135            140
226     cct ttc tgt agc tat gct tgt aga aga agg gac gct ctc aca gga cac     480
227     Pro Phe Cys Ser Tyr Ala Cys Arg Arg Arg Asp Ala Leu Thr Gly His
228         145            150            155            160
229     ctc agg acc cat tct gtg ggt aaa cct cac aag tgt aac tac tgt ggc     528
230     Leu Arg Thr His Ser Val Gly Lys Pro His Lys Cys Asn Tyr Cys Gly
231         165            170            175
232     cga agc tac aag cag cgc acg tca ctg gag gaa cac aag gaa cgc tgt     576
233     Arg Ser Tyr Lys Gln Arg Thr Ser Leu Glu Glu His Lys Glu Arg Cys
234         180            185            190
235     cac aac tat ctc cag aat gtc agc atg gag gct gcc ggg cag gtc atg     624
236     His Asn Tyr Leu Gln Asn Val Ser Met Glu Ala Ala Gly Gln Val Met
237         195            200            205
238     agt cac cat gta ccg cct atg gaa gat tgt aag gaa caa gag cct atc     672
239     Ser His His Val Pro Pro Met Glu Asp Cys Lys Glu Gln Glu Pro Ile
240         210            215            220
241     atg gac aac aat att tct ctg gtg cct ttt gag aga cct gct gtc ata     720
242     Met Asp Asn Asn Ile Ser Leu Val Pro Phe Glu Arg Pro Ala Val Ile
243         225            230            235            240
244     gag aag ctc acg gca aat atg gga aag cgc aaa agc tcc act cct cag     768

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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text
